

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGGAATTTCGGTGGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCAGCGGATCGGCTTCGCCATCGCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAATGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGTGTTCTCTGC
ATTCACCCACTGGCCTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCTTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGTCT
GTTGTTGTGECCTTGGGTAAAGGCCTCCCTGAGAACACAGGACAGGCCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVVV
SRKQQNVDAQAVATLQGEGLSVTGTVCVHGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNCIAPGLIKTSFSRMLWMDKEEESMKETLRIRRLGEPEDC
AGIVSFLCEDASYITGETVVVGGGTPSRL

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCTCCGGCCCGATAGCGGCATCGAGAGCGCTCCGTGAGGACCAAGCGCGC
CAGGGGGCCGGCGGCGAAAGGAGATGAGGGGGCGCAGCAGCTGTGACCTTGCCAGAACCGAGTGGC
GCGGCTGGAGGAGGAGAACCGAGACTTCTGGCTGCGCTGGAGGACGCGCTGAGCAGTACAACTGC
AGAGCGACCGGCTCGCTGAGCAGCAGGAGGAGATGGTGGAACTCGGGCTCGGGTTAGAGCTGTGTCGG
CCAGGCTGGGGGGCTCGGGCTCTGAACTGGCCTGCGCTCCGGGTCTTTGTGCTTCGACCTCATAC
AGCCCCCTGGGGGGTGCCACGCCCCATGTGCTGGGCATGGTGCCGCTGCGCTGCCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCGCC
CAGGCGGACCTTACACTGCGCAGAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCAGCCCCAG
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCTTGAGGAGTTGGATGACAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCGAGTTTCAGGCCCGCAGGTCCCGCTGCCACAGCCCTCAGAGTG
GCGGCTGGCCCGAGCCAGCAGAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTCGGGAGCT
CGAGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGACAGGAGGGTTCGTG
CGGCCAGAGCCAGGTGCAAGTGTCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTCTG
GCCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGACA
GCTGTCAGAGCGGCTTCGCGAGGAGACGGAGCAGAAAGCGCGCTGGAGGACAGAAATGAGCAAGCGGC
AGCACGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAAGCAGAAATCTCGAAGATTAAAGACGGAA
GAGATCGCGGCTTCAGAGGAAGAGGGCGAGTGGCAGCAACGGCTCTGTGGTTCAGCCTGGAACAGCA
GCGAAGATTGAGGAGCAGAAAGTGGCTGACAGGAGATGGAGAAGTGTACAGCAGCCGGCGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAGAGGAGGCGCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCTGAGATCCAGCCAGGCCCTCAACAGGACATCGTGC
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGTGTCCGAGAAGAGCGGGCAGCTGCGGCAAGGCA
CGGCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAGAAGACTCGTGTCT
AAGCAGCGCTGGAGATCGACGCGAAGCTGAGGCGAGGGAGTCTGTCTGCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCAGGCGCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCGCAGCGGGTGCCTTCGGGCCCTCAGCCTCGTTGTCTGTGCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCTCAGAGACGAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCGCAGCAGATTGCCCTTCTCGGAATCGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACTGCAGTGTCTCCTGCAGCAGAGTCAGAGACCACTCGGTGA
AGGGTTAGCAGCAGCAGGAGGAGTATGAGGCCCGGATTCAAGCTCTGGAGAGGAACTGGCGCGTT
ACATGTGGATAAACAGGAACCTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
GGGGAGAAGAGGAGCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTTGGC
ACCCGAGCTTCTGCTGTTCGGCTCTCAGTGAGGGGGCCCCCGCACCGGGAGGAGACCGGGACT
TGGTCCACGCTCGGTTACCTTGACCTGGAACGCTCGAGCCTGTGTGGTGGAGAGCAGGGGTCCCC
GAGGAATGAGGCAGCGGGAGGCGGCTGAGCCCTGGTGGGGCGGGTCTTCTGTGGGTGGAGCAGG
CCTGCCCTGGAACTTTGGGCACTTTGTCCAAGCCCGGGGAACTGCGACAGGAGCCAGCTCGGAGTGA
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGAGACCTGCCCTGGAGGAGAGCTCCGAGCT
GCTGAAGGGGCGAGCTGCTGTTTTGCTTCTGTGAAGGCGAGTCTTACCAGCACACCTTAATCCAGG
CCCTCATCTGTACCCCTCACTGGGATCAACAAAATTTGGGCCATGGCCCCAAAGAACTGGACCTCATTT
AACAAAATAATATGCAAAATCCCACTACTTCCATGAAGCTGTGGTATCCCAATTCGCGCCTTGTG
TCTTGTCTGCAATCTCAGACAATCTGCTTTTCAGGCGTAAATGGATGTGCTTGTAGTTGAGGGGTTTG
GCCAAGAAATCATCAGAAAGGGTTCGTGGCAACAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAACTGGGAGCTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

10033221-4422001

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLSQSDRLREQQEEMVELRLRLELVPRPGWGGLRLNLPGPSFVPRPHTAPLGGAHAHV
LGMVPPACLPGEDEVGSEQRGEQVTNGREAGAELLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAAQQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAQSQVQLKEKKQATERLVLSAQSEKRLQE
LERNVQLMRQQGQLQRRLEETEBOQRRLEAEMSKRQHRVKELELKHEQQQKILKIKTEBIA
AFQRRRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLHLEKELSEKSGQLRQGSQSQQQIRGEIDS
LRQEKDSSLKQRLIEDGKLRQGSLLSPPEERTLFLQLEDAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCYFDKVVTLREEHQHQQIAFSELEMQLEEQQR
LVYVLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGEEKRSLCSEGRQAPGNEDELHLAPPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTCTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCCTTCCAGCTCCCCCTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTACCATCT

100344-12701
0221-4422001

FIGURE 6

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQCSKGTDDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPISRCTRNRRLHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCACGCGTCCGCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCTCCGCGGAGAGGAGCGAGGCGCGCCAGGGTGCCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTAGTGGTCCGCCCCACGCGGG
TCGCGGCGCGGCCAGGATGGGCGCTGGCAACCGGGCCCGCGCCCGCTGCTACCCCTG
CGCCCGCTGCGAGCCGCGCTCCGGCCCCGCGCCTGCGCTCATGGACGCGGGTCCCGGCTG
GCGGCGCGCGCCCCGGGGTGTGAATGCGACTCGCCCCCTCGGCGCGCTCCCGCCCGCCC
GCGCGCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCACGACACAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCGAGCGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCAGGGCGGGGCGCCAAGGCCGGGATCTGCGAGGTCCGGCCCCCGGGGACAC
CCCGCAGCGGAAGCCTTGCCCGCAGCCGCCAGGACGCGATTGGCCCGGAACCTCGCGCCCA
CGCCGAGCCACCCGAGGAGTACGTGTACCCGACTACCGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTGCGCGCGGGCCCCCTCGGCCTGCCGTGCCT
GTGCACCGAGGAGGGGCGCGTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTCGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
CGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAAACGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCTGATCAGTGCTGTCCATCTGCAAAAATGGTCCAACTGCTTTTGAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
TTATGAGGAAGGCATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCAGAAACAAAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA
CATTCTAGATGACTCTGGGAACATCAGTCAAGAAGACTTTTGATGAGGAATAATGGAAAA
TGTGTGGTACTTTTCTTTTCTTGATAACAGTTACTACAACAGAAGGAATGGATATATTTT
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTGTCAACCGTCAAAAAA
AAAAAAAAAAAAAAAAAAAA

10332412701

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818
><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALA
AAAQDAIGPELAPTPEPPEEYVYPDYRGKGCVDSESGFVYAIGKEKFAFGPSACPLCTEEGPL
CAQPECPRHLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVS PCERCRC EANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETA VIPAGREVKTD ECTICHCTYBEGTWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

10033244.12701

FIGURE 9

CAGCCACAGACGGGTATGAGCGGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGGTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCTATCGGGGACCACATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTGAGGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCTGGG
GTGCTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCCGTCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
GAGCATTAGGGCTGCGTGGCCCAACCTTCAGCTTCTTGTGTAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGAGGT
GGGGCTGAGGGCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGGTTTGCCCTTCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACAATCATTCATATCTACTCACCTAACAGCA
ACACTGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847
><subunit 1 of 1, 437 aa, 1 stop
><MW: 46363, pI: 6.22, NX(S/T): 3
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ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGGGIFSNLRVQGCMPPQGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAFPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGACCTCCGTAGCGCTGCCGCGGCCCTG
GCTGCGGCGCTGCTCTCGTGCCTTGCGCGCTGCTCTCTTAGAGCCGAGGGACCCGGTGGC
CTCGTCTGCTCAGCCCCATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGTGGTGCGCCCTCATTGCGCCACGGCACCCGCTACCCACGGTCAAACAGATCGCGAAGCT
GAGGCAGCTGCACGGTTGCTGCAGGCCCGCGGCTCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCCGCAGCTGGGTGCAGCGCTGGCCGACTGGCCCTTTGGGTACCGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCCGCTGCGGCTCATCACAGTTCGAAGC
ACCGCTGCATGGATAGCAGCGCCGCTTCTCGAGGGGCTGTGGCAGCACTACCACCTGGC
TTGCCGCCCGCGGACGTCGCAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTGATCACTGTGAGAAGTTTAACTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCAGTGGAAAGCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTAAATGCAGATTAAATCAAGTAGCCTTTTTCACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTGACATAGATG
ATGCAAAGGTATAGAATATTTAAATGATCTGAAACAATATTTGAAAAGAGGATATGGGTAT
ACTATTACAGTGCATCCAGCTGCACCTTGTTTCAGGATATCTTCAGCACTTTGGACAAAAGC
AGTTGAACAGAAAACAAAGGTCTCAGCCAATTTCTTCCAGTCACTCCAGTTTGGTCATG
CAGAGACTCTTCTCCACTGCTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCGGAAGTGGTCTCATTTGATACCTTATGC
CTCGAACCTGATATTTTGTGCTTTACCACTGTGAAAAATGCTAAGACTCCTAAAGAACAAATCC
GAGTGCAGATGTTATTAAATGAAAAGGTGTACCTTTGGCTTACTCACAGAAACTGTTTCA
TTTTATGAAGATCTGAAGAACCCTACAAGGACATCCCTCAGAGTTGTCAAACCAAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACATGAGTAACTGAAGAACATTTTT
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGAATAGGTAGGCAATTCCTTGATT
ACAGGAAGCTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAAGAAAAGATTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAAATGTTTACAGAAATGAAATCTTCTCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTTATAATAACACTTGAAGAGTGCT
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AGATTGTTCTGCAGTTCCTCTCTCTTTTCTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
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TTGAAACAAGAAACAGAGTGTGTGAAAAGGACACCTTCAC'TGAAGCAAGTCGGAAAGTACAA
TGAAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTCAATCTGT
CACTTGGCTTCGATTTTTATATTTTCTATATATGAAATGATCTTTTGGTTGTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATCTTGTGACTTTAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

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GPEAPWRDPPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPDPVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLIFVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC
 TCCGGCTTCGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCGTATAGGGGCTGTAAATC
 TCAAAATCCAGCAATCGAACCCGATGGTACAGAGAAATTTGAAAGTGTGGAACTGTCTTGCATCATACGGATTTCGC
 AGACAAGTGACCCAGGATCGAGTGGGAAGAAATTTCAAGATGAACAAACACATATGTGTTTTTGACAAACAAA
 TTCAGGGAGACTTGGGGGCTGTCGAGAAATACTGGGGAAGACATCCCTGAAGATGTGACACAGGAGAG
 ACTCAGCCCTTTATCGCTGTGAGGTGTCTGCTCGAAATGACCGCAAGGAAATTTGATGAGATTTGTGATCGAGTTAA
 CTGTGCAAGTGAAGCCAGTGCACCTGCTGTGTAGAGTGCAGAGGCTGTACCAAGTGGCAAGATGGCAACACTGC
 ACTGCCAGGAGAGTGGGGCCACCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACCGGATT
 CCAGAGCCAAATCCAGATTTGCGAATTTCTTCTTCCACTTTAAACTCTGAAACAGGCACTTTGGTGTCTACTGCTGT
 TTCACAAAGCAGACTCTGGGCGAGTACTGTGCAATGTCTTCAATGACGCGAGCTCAGCCAGGTGTGAGGAGCAGG
 AGATGGAAGTCTATGACTGAACATTGGCGAAATTTATGGGGGGGTTCTGGTTGTCTTGTGCTACTGGCCCTGA
 TCACGTTGGGCATCTCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
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 GGAAGCGAAATCTGGGTGCGTTCTGAGTGGGTTCTTAATCTGTTTCTGGGCTGACCTTCCGCGATGAGTATGAG
 GTGATCTTAAAGAGTTTGTCTCAGTAAACGCCCTGTGCTGGGCCCTGTGAAGCCAGCATGTTTACCACCTGGTCTGT
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 GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTCTTAAAGGCTCTGC
 TGATCGGTTGTGAGTGTCCATTTGTGAGAGAAGCTTTTGGATCAGCAATTTGTAAAAACAACAAAATCAGGAAG
 GTAAATGGTTGCTGGGAAGGGATCTTGCCTGAGGAACCTCTGTTGTCCAAAGGGGTGCAAGATTGAAGAAA
 ACCTTCGCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
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 TGGAAAAATCAATAATTAAGAGTATTTTACCACAGGAATCTCTCATGGAAGTTTACTGTGATGTTCTCTTTCT
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 TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTTAGCTTTGAAC
 GCCTCTTCTCGAGATGACTAGGACAGCTGTATCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
 CCAGTCAGCTCTCGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCTCTGCTGTGCGCAGGAGGCCCT
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 TCTCAGGTTGGGCACTCGAGGACACTGGTGTCTTCCATGTAGCTGCCAGTCTGGGCTCCTGTAACAGACCTCT
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 GGAATGCTCCAGCAGTGGCTCAGTGTCTCCTGGTGTCTGCTGCATGGCATCTGGATGCTTAGCATGCAAGTTC
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10033244.12701

FIGURE 14

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><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
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PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG
VLVVLAVLALITLIGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTCTTCTACGCTGGAGCAGCGGGGAGACAGCCACCTGACACATCTCTGGTCCATGCCATGGTG
 ATCTCTGCTGACGCTGGGCCCGCTCTGAGCCGACGACAGCGAGTTCAGGCGCTGCTGGACATCTGTTTTCGGAG
 GAGAAGCCATGCCACCGCCTTCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCTGACTGGCTGAAGCTG
 GCTGATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCGCCCTGCAGGACCTGGAGCCGACAGCAGCTGCTGTG
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 GACCCCCAGACTCTGGAGCAGAAACATCATGGACAAGAAATACATGGCCACCTGTGGAGGTCTGCAGCATGAGCGC
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 GGCAAAGGTCAAGCCAGCGTGCCTCGTTCCGTCCCTACCTCTGACCTCTTACGCATCAGTCCAGCTGGCCC
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 TTCTCTGGGCTGCATCCATGTTCTCTGCATCTGGCAGGGGGGGACAGCGCACCCCGCAGAGCGGGGGAG
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 GACGATGAGAGTGTCAAGGAAGTGACGGAGCACCTGTCAAGGTGCATCCAGCAGTGGGGAGACAGCGTGTCTGGGA
 AGGCGCTGCCAGACTTCTCTGCACTCTACCTACAGCGGCCGAGCTGCGGCTGCCCGTGGCTGAGGTCTCTA
 CTGCAACAGCAAGGGCTGCCAGCAGCAGCTGTGCAAGCTGGAGGACTCATCCACCGCTTCATACCGCTCTCT
 CGGACACCGCACTCCCGGCGTTGGAGAACCAGAGGGCGGATGCCAGATGGCTGCCGGAAGCTGGCGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACTGCCATGATCGCGCGCTCTGCACGCGCCACCCACCTCAACTTC
 CAGGAGTTCGGGACAGCAACACCTGAGCTGCTTCTGCACTGCTGGGCTGCTGGAGTGTCTGCAGCCGCAC
 GTGTCTCCGACGGAGCACAGGGGGCGCTGTGGACTGCTTCTGCTCTTCTCCGCTGCTGTGATTAATCAGG
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 GCGGAGGAGGAGGAGCTCTGCGGCTCTTGCCTGTGTCAGCTCTCCCTCTGACCCCTCTGACCCGCGGCGAG
 ATGGCCCCCTACATGAAACGGCTTTCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGCTCCGGCGAGACCGAGGAGATCTGAGCTTCTCTCGACCACTGCAGCGGCTGATGAGCTCGGCGAG
 GAGTGTGTGCGCAACTCTCGCCTTCACTGCTGGCCTGCGCTCCAGCAGACAGCCGACATTTGCAGCGCTTCT
 CTGCCACGTTTCATGTACTGCTTGGGAGCAGGAGCTTTGAGGTGGTGCAGACGGCCCTCGGGAACCTGCTGAG
 TACGCTCTCTGTGCGCAAGAGCAGCGGCTGTGCTGCTCCACCGGCCCTCTCTGTGGGCTGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCTGCATATGAGAGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCTCTCAAGCCCCGGCCGCTCCGCTCCCGGGATCTCGAGGCAAGGCCAGGAGCGTGGGCTGTGCTG
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 CTCCGGGCGCGGCTGGCATAGGGGCCGTCCAGCAAGCCCTCATTCACCTCTGGGCGACAGCCCTGCGCGG
 AGCGGCGGATCCCCCGGCATGGCTGGCTGGTGTGTTTGAATGAAACGACCTGAACTGTCAA

Time (min)	Temperature (°C)	Pressure (atm)	Flow rate (mL/min)	Wavelength (nm)	Detector (nm)	Sample (mg/mL)	Concentration (mg/mL)	Volume (mL)	Mass (mg)	Yield (%)
0	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
10	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
20	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
30	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
40	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
50	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
60	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
70	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
80	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
90	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
100	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
110	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
120	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
130	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
140	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
150	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
160	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
170	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
180	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
190	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
200	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
210	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
220	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
230	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
240	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
250	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
260	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
270	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
280	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
290	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
300	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
310	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
320	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
330	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
340	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
350	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
360	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	100
370	25	1.0	1.0	254	254	0.1	0.1	1.0	0.1	

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

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MAHLVEVQHERGASGGQTFHSLLTASLPPRDSTAPKPKSSPEQPTGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDRWQSSSRPVVALAQALQQLARVVQGSPEVPGITVRVLQAL
ATLSSPHGAQLVMSMRHSFPLACPLLRLQLCQYQRCVPQDTGFSSFLKVLLLQMLQWLDSPG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLLRLAEALAFQDLEVSSTRAVITLRSGEQ
CSVEPDLISKVLQGLIEVRSHPLEELLTAFPSATADAASPPACKPVVVSSLLLQEEBPLA
GGKPGADGGSLEAVRLGSPRLVLVDVLEMLDPEVVSSCDPLQRLRLFSRRKGKGQAVPSFR
PYLLTLFTHSWPTLHQICIRVLLGKSREQDFPSSASDLQACHIVPRIWGGRDQRTPOKR
REELVRVQGPESLISVELILAEATRSQDGTAACSLIQARPLLSSCCGDDESVRKVTE
HLSGCIQQWGDSDLGRRCRDLLLLQLYLQRPELVRVPVEVLLHSEGAASSVCKLDGLIHRFI
TLTADSDSRALENRGADASMACRKLAVAHPLLLRLHPMIAALLHGRTHLNFQEBQRQNHLS
SCFLHVLGLLELLQPHVFRSEHGQALWDCLLSFIRLLNPKRSCSRHLAEIFKNKFVFIKXYI
TYNAPAAISFLQKHADPLHDLSDFNDSLDVMLKSLLAGLSLPRSDRDTGRDLEEGEESAG
SLPLVSVSFLTPTATAEMAPYMNKSLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL
MSSAECCRNLAFSLALRSMQNSPSTIAAFLPTFMYIKSGQSDFEVVQTLRNLPEYALLCQE
HAAVLLHRAFLVGMYGMDPSAQISEALRLIHEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

FIGURE 17

CCGGGCCATGCAGCCTCGGCCCGCGGGCGCCCGCGCGCACCCGAGGAGATGAGGCTCCGC
AATGGCACCTTCTCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCTCTCGCTGTCTGGTA
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GTGCTGGACGAGATCAAGAGGGCCGTGTGAGAAAGCAGGCGCTGCGAGACGGAGACGGCAA
TCGCACCTGGGGCCGCTTAACAGAGGACCCCGATTGAAGCCGTGGAAACGGCTCACACCGGC
ACGTGCTGCACCTGCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCGCGGTGCGCTGGGGCAGGGCCGACCCGGAGTGTCCGTGGTGATGGGCATCCC
GAGCGTGCGGCGGAGGTGCACTCGTACCTGACTGACACTCTGCTACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAAGGAGACTCGGTATCTGTGGTGCTGATCGCCGAGACTGACTCACAG
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CCTGGAGGTTCATCTCACCTTCCCCCACTTCTACCTTGACTTCTCCCGCTCCGAGAGTCTCT
TTGGGGACCCCAAGGAGAGAGTCAAGTGGAGACCAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCCAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACCTGAGCACCATGAAGAACTTGCAGCTGACGACGCTTCAGAGGACTGGATGA
TCTTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGAGCTGAGCCTG
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ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACCTCACTCCTCGCTGGCT
GGCAAGATCCAGAAACTGAAGGACAAAGACTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATACCAGCACTTCACCTTGGAGAAAG
CCTACCTGCGCGAGGACTTCTTCTGGGCTTCAACCTGCGCGGGGGGACTTCATCCGCTTC
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTCCGCACTGGGAACATCGAGCACCC
GGAGGACAAGCTCTTCAAACAGTCTGTGGAGGTGCTGCCCTTCGACAACCTCAGTCAGACA
AGGAGGCGCTGCAAGGAGGGCCGCAACGCCACCTCCCGTACCTCGGAGACCCCGACGGCTAC
CTCCAGATCGGCTCCTTCTCAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC
TCTGGAAGCACTGCGCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCCGACTTAAGCTGCGGGCTTCTGAGGGTACCTGTGGCCAGCCCTGAA
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AGGGTTCTGCTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCGCTGGCCCGGAGGCCCTA
GGAGCTGGTGCTGCCCCCGCCCGCGGGCCGCGAGGAGGAGGCGGCCCCACACTGTGCC
TGAGGCCCGGAACCGTTTCGCACCCGGCTGCCCGAGTCAGGCCGCTTTTGAAGAGCTTTTAC
TTGGGCGCCCGCGTCTTGGCGCGAACACTGGAATGCATATACTTTATGTGCTGTGTT
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ACTTGTAAATAAAGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 18

```
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><subunit 1 of 1, 548 aa, 1 stop
><MW: 63198, pI: 8.10, NX(S/T): 4
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ELNLVLDEIKRAVSEKQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFHHLPHLLA
KESSLQPAVRVGGQRTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSHPFYPDFSRLRESFGDPKERVVRWRTKQNL
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DLSLIVEFILMFYRDKPIDWLLDHILWVKCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515